



## SEQUENCE LISTING

<110> Kauppinen, Markus Sakari  
Schulein, Martin  
Schnorr, Kirk  
Andersen, Lene Nonboe  
Bjornvad, Mads Eskelund

<120> Novel Mannanases

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<140> 09/339,159

<141> 1999-06-24

<150> 60/106,054

<151> 1998-10-28

<150> 60/105,970

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<150> 60/123,543

<151> 1999-03-09

<150> 60/123,623

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 <213> Bacillus sp. I633

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 Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn Gly  
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 Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp Asp  
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 Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Gly  
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 Gly Thr Ser Pro Thr Thr Leu Tyr Asp Phe Glu Gly Ser Met Gln Gly  
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 Trp Thr Gly Ser Ser Leu Ser Gly Gly Pro Trp Ala Val Thr Glu Trp  
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 Ser Ser Lys Gly Ser His Ser Leu Lys Ala Asp Ile Gln Leu Ser Ser  
 370 375 380  
 Asn Ser Gln His Tyr Leu His Val Ile Gln Asn Thr Ser Leu Gln Gln  
 385 390 395 400  
 Asn Ser Arg Ile Gln Ala Thr Val Lys His Ala Asn Trp Gly Ser Val  
 405 410 415  
 Gly Asn Gly Met Thr Ala Arg Leu Tyr Val Lys Thr Gly His Gly Tyr  
 420 425 430  
 Thr Trp Tyr Ser Gly Ser Phe Val Pro Ile Asn Gly Ser Ser Gly Thr  
 435 440 445  
 Thr Leu Ser Leu Asp Leu Ser Asn Val Gln Asn Leu Ser Gln Val Arg  
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 Ser Ile Tyr Ile Asp Asn Val Ile Val Glu  
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 <213> Bacillus sp. I633

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 gaagggattg caaataccgg tgctaatacgt gtcgggattg tggtatctga tgggggacaa 180  
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 gctgcggggg ggggacaatt tccacaatcg attcatgatt atggaagaga agtttttaat 540  
 gctgaccctc aacgaaatac aatgttttcg attcatatgt atgaatatgc aggtggtaat 600  
 gcatcgcaag ttctactaa tattgaccga gttcttaatc aagacctcgc attagtcatt 660  
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 Asn Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp  
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 Asp Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His  
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 Leu Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp  
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 Phe Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala  
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 Ala Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg  
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 Asp Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly  
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 His Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr  
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 Gly Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn  
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Gln Phe Lys Val Thr Asn Thr Gly Ser Ser Ala Ile Asp Leu Ser Lys  
340 345 350

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Phe Trp Cys Asp His Ala Ala Ile Ile Gly Ser Asn Gly Ser Tyr Asn  
370 375 380

Gly Ile Thr Ser Asn Val Lys Gly Thr Phe Val Lys Met Ser Ser Ser  
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Leu Glu Pro Gly Ala His Val Gln Ile Gln Gly Arg Phe Ala Lys Asn  
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Asp Trp Ser Asn Tyr Thr Gln Ser Asn Asp Tyr Ser Phe Lys Ser Arg  
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 Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly  
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 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met  
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 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu  
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 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr  
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 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala  
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 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp  
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 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met  
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 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp  
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 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
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 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser  
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 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser  
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 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His  
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 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln  
  305                  310                  315                  320

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Pro	Glu	Pro	Pro 340	Thr	Ala	Thr	Thr	Leu	Tyr 345	Asp	Phe	Glu	Gly 350	Ser	Thr
Gln	Gly	Trp 355	His	Gly	Ser	Asn	Val 360	Thr	Gly	Gly	Pro	Trp 365	Ser	Val	Thr
Glu	Trp 370	Gly	Ala	Ser	Gly	Asn 375	Tyr	Ser	Leu	Lys	Ala 380	Asp	Val	Asn	Leu
Thr 385	Ser	Asn	Ser	Ser	His 390	Glu	Leu	Tyr	Ser	Glu 395	Gln	Ser	Arg	Asn	Leu 400
His	Gly	Tyr	Ser	Gln 405	Leu	Asn	Ala	Thr	Val 410	Arg	His	Ala	Asn	Trp 415	Gly
Asn	Pro	Gly	Asn 420	Gly	Met	Asn	Ala	Arg 425	Leu	Tyr	Val	Lys	Thr 430	Gly	Ser
Asp	Tyr	Thr 435	Trp	His	Ser	Gly	Pro 440	Phe	Thr	Arg	Ile	Asn 445	Ser	Ser	Asn
Ser	Gly 450	Thr	Thr	Leu	Ser	Phe 455	Asp	Leu	Asn	Asn	Ile 460	Glu	Asn	Ser	His
His 465	Val	Arg	Glu	Ile	Gly 470	Val	Gln	Phe	Ser	Ala 475	Ala	Asp	Asn	Ser	Ser 480
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<212> DNA
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 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met  
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 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp  
  225                  230                  235                  240  
 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
           245                  250                  255  
 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser  
           260                  265                  270  
 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser  
       275                  280                  285  
 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His  
   290                  295                  300  
 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln  
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[illegible]

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<211> 1761
<212> DNA
<213> Bacillus halodurans
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caaaacgcgt	ctcaattatg	aaaagagttg	tttgcttttt	tacgtgatgt	aagtggtaaa	180	
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caagaacaaa	gaatcttaaa	tacagcagat	tcaattgaag	cagctcacga	cttaggtgtgg	420	
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1761

&lt;210&gt; 10

&lt;211&gt; 586

&lt;212&gt; PRT

&lt;213&gt; Bacillus halodurans

&lt;400&gt; 10

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Ile Phe Pro Ser Thr Ser Phe Ala Phe Ser Gly Ser Val Ser Ala Ser  
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Gly Gln Glu Leu Lys Met Thr Asp Gln Asn Ala Ser Gln Tyr Thr Lys  
 35 40 45

Glu Leu Phe Ala Phe Leu Arg Asp Val Ser Gly Lys Gln Val Leu Phe  
 50 55 60

Gly Gln Gln His Ala Thr Asp Glu Gly Leu Thr Leu Arg Gly Thr Gly  
 65 70 75 80

Asn Arg Ile Gly Ser Thr Glu Ser Glu Val Lys Asn Ala Val Gly Asp  
 85 90 95

Tyr Pro Ala Val Phe Gly Trp Asp Thr Asn Ser Leu Asp Gly Arg Glu  
 100 105 110

Lys Pro Gly Asn Asp Glu Pro Ser Gln Glu Gln Arg Ile Leu Asn Thr  
 115 120 125

Ala Ala Ser Met Lys Ala Ala His Asp Leu Gly Gly Ile Ile Thr Leu  
 130 135 140

Ser Met His Pro Asp Asn Phe Val Thr Gly Gly Ala Tyr Gly Asp Thr  
 145 150 155 160

Thr Gly Asn Val Val Gln Glu Ile Leu Pro Gly Gly Ser Lys His Glu  
 165 170 175

Glu Phe Asn Ala Trp Leu Asp Asn Leu Ala Ala Leu Ala His Glu Leu  
 180 185 190

Lys Asp Asp Asn Gly Lys His Ile Pro Ile Ile Phe Arg Pro Phe His  
 195 200 205

Glu Gln Thr Gly Ser Trp Phe Trp Trp Gly Ala Ser Thr Thr Thr Pro  
 210 215 220

Glu Gln Tyr Lys Ala Ile Tyr Arg Tyr Thr Val Glu Tyr Leu Arg Asp  
 225 230 235 240

Val Lys Gly Ala Asn Asn Phe Leu Tyr Gly Phe Ser Pro Gly Ala Gly  
 245 250 255

Pro Ala Gly Asp Leu Asn Arg Tyr Met Glu Thr Tyr Pro Gly Asp Asp  
 260 265 270

Tyr Val Asp Ile Phe Gly Ile Asp Asn Tyr Asp Asn Lys Ser Asn Ala  
 275 280 285

Gly Ser Glu Ala Trp Ile Gln Gly Val Val Thr Asp Leu Ala Met Leu  
 290 295 300

Val Asp Leu Ala Glu Glu Lys Gly Lys Ile Ala Ala Phe Thr Glu Tyr  
 305 310 315 320  
 Gly Tyr Ser Ala Thr Gly Met Asn Arg Thr Gly Asn Thr Leu Asp Trp  
 325 330 335  
 Tyr Thr Arg Leu Leu Asn Ala Ile Lys Glu Asp Pro Lys Ala Ser Lys  
 340 345 350  
 Ile Ser Tyr Met Leu Thr Trp Ala Asn Phe Gly Phe Pro Asn Asn Met  
 355 360 365  
 Tyr Val Pro Tyr Lys Asp Ile His Gly Asp Leu Gly Gly Asp His Glu  
 370 375 380  
 Leu Leu Pro Asp Phe Ile Lys Phe Phe Glu Asp Asp Tyr Ser Ala Phe  
 385 390 395 400  
 Thr Gly Asp Ile Lys Gly Asn Val Tyr Asp Thr Gly Ile Glu Tyr Thr  
 405 410 415  
 Val Ala Pro His Glu Arg Leu Met Tyr Val Leu Ser Pro Ile Thr Gly  
 420 425 430  
 Thr Thr Ile Thr Asp Thr Val Thr Leu Arg Ala Lys Val Leu Asn Asp  
 435 440 445  
 Asp Asn Ala Val Val Thr Tyr Arg Val Glu Gly Ser Asp Val Glu His  
 450 455 460  
 Glu Met Thr Leu Ala Asp Ser Gly Tyr Tyr Thr Ala Lys Tyr Ser Pro  
 465 470 475 480  
 Thr Ala Glu Val Asn Gly Gly Ser Val Asp Leu Thr Val Thr Tyr Trp  
 485 490 495  
 Ser Gly Glu Glu Lys Val Gln Asp Glu Val Ile Arg Leu Tyr Val Lys  
 500 505 510  
 Ala Ser Glu Ile Ser Leu Tyr Lys Leu Thr Phe Asp Glu Asp Ile Asn  
 515 520 525  
 Gly Ile Lys Ser Asn Gly Thr Trp Pro Glu Asp Gly Ile Thr Ser Asp  
 530 535 540  
 Val Ser His Val Ser Phe Asp Gly Asn Gly Lys Leu Lys Phe Ala Val  
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 Asn Gly Met Ser Ser Glu Glu Trp Trp Gln Glu Leu Lys Leu Glu Leu  
 565 570 575  
 Thr Asp Leu Ser Asp Val Asn Leu Ala Lys  
 580 585

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 <212> DNA  
 <213> Bacillus sp. AAI12

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 ggggttttaa atacttcttc ttcacaagca gaagcccatc acagtgggtt ccatgttaat 120  
 ggtacaacat tatatgatgc aaatggaaac ccttttggtta tgagagggat taatcatgga 180  
 catgcttggt ttaaacaaga actagaaaca tccatgagag ggattagtca aacaggggca 240  
 aatacgattc gtgtcgtttt gtctaattggg caaagatggc aaaaagatga tcgaaacatg 300

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gtagcttcgg ttatttcttt ggcagagcag catcaaataa ttgccgtttt agaagttcat 360
gatgctactg gtagcaataa tttctccgat ctgcaagctg ctgtggacta ttggattgag 420
atgaaggatg ttttgcaggg gaaagaggac atagtgatca ttaatatcgc caatgaatgg 480
tacggtgctt gggacggagg cgcattggga cgagggtatc agaatgcgat acgtcagctt 540
cgaaatgcag gcttgtcaca tacatttatg gttgacgctg ccggttatgg ccagtaccct 600
caatcggtag ttgattatgg tcaagaagta ttaaattgctg acccacagag aaacacaatg 660
ttttctgttc atatgtatga atatgcaggc ggagatgcta atacagtaag acgaaacatt 720
gactcgatct taagccagaa cttagctctt gtcattggtg aattcgggca ttggcattat 780
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<210> 12

<211> 331

<212> PRT

<213> Bacillus sp. AAI12

<400> 12

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His His Ser Gly Phe His Val Asn Gly Thr Thr Leu Tyr Asp Ala Asn
      35                      40                      45

Gly Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Phe
      50                      55                      60

Lys Gln Glu Leu Glu Thr Ser Met Arg Gly Ile Ser Gln Thr Gly Ala
      65                      70                      75                      80

Asn Thr Ile Arg Val Val Leu Ser Asn Gly Gln Arg Trp Gln Lys Asp
                85                      90                      95

Asp Arg Asn Met Val Ala Ser Val Ile Ser Leu Ala Glu Gln His Gln
      100                      105                      110

Met Ile Ala Val Leu Glu Val His Asp Ala Thr Gly Ser Asn Asn Phe
      115                      120                      125

Ser Asp Leu Gln Ala Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Val
      130                      135                      140

Leu Gln Gly Lys Glu Asp Ile Val Ile Ile Asn Ile Ala Asn Glu Trp
      145                      150                      155                      160

Tyr Gly Ala Trp Asp Gly Gly Ala Trp Ala Arg Gly Tyr Gln Asn Ala
      165                      170                      175

Ile Arg Gln Leu Arg Asn Ala Gly Leu Ser His Thr Phe Met Val Asp
      180                      185                      190

Ala Ala Gly Tyr Gly Gln Tyr Pro Gln Ser Val Val Asp Tyr Gly Gln
      195                      200                      205

Glu Val Leu Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Val His
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Met Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Arg Asn Ile
      225                      230                      235                      240

Asp Ser Ile Leu Ser Gln Asn Leu Ala Leu Val Ile Gly Glu Phe Gly
      245                      250                      255

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His Trp His Tyr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr  
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Ser Gln Gln Arg Asn Val Gly Trp Leu Ala Trp Ser Trp His Gly Asn  
 275 280 285

Ser Glu Gly Val Glu Tyr Leu Asp Leu Ser Asn Asp Phe Ala Gly Asn  
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Arg Leu Thr Trp Trp Gly Asp Arg Ile Val Asn Gly Pro Asn Gly Ile  
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Arg Gln Thr Ser Lys Arg Ser Ser Val Phe Gln  
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 <211> 1464  
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 <213> Humicola insolens

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 agtgacaaga tcacgttcca cgtggacagc gagaccacac ggctgtacga cctcaccatc 300  
 cgcggtggccg ccatctatgg cgagaagcgc accaccgtcg tgctcaataa cggcgcgcca 360  
 agtgaggtct acttcccggc aggcgattcg ttcgtcgaca tcgctgccgg ccaggtcctg 420  
 ctgaaccagg gcgacaacac catcgacatt gtcaacaact ggggatggta cctgatcgac 480  
 tccatcacca tcacccctc cgccccgcga cccctcacc aaatcaacc ttcccccgctc 540  
 aacctgccc cgcagacaaa cgcgcggcg ttgtacgcat acctccgctc catctacggc 600  
 aagaaaaatcc tttccggcca gcaggagctt tcctgggcca actggatcgc ccaacagacg 660  
 ggcaaaactc ccgcgctggt gtccgtcgat atgatggatt attcccctag tcgggtggaa 720  
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 <211> 488  
 <212> PRT  
 <213> Humicola insolens

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Ser Gln Glu Pro Thr Ser Thr Pro Ser Pro Val Pro Gly Pro Arg Thr  
 35 40 45

Phe Glu Ala Glu Asp Ala Ile Leu Thr Gly Thr Arg Val Glu Ser Ser  
 50 55 60

Leu 65	Ala	Gly	Tyr	Ser	Gly 70	Thr	Gly	Tyr	Val	Ala 75	Gly	Phe	Asp	Glu	Pro 80
Ser	Asp	Lys	Ile	Thr 85	Phe	His	Val	Asp	Ser 90	Glu	Thr	Thr	Arg	Leu 95	Tyr
Asp	Leu	Thr	Ile 100	Arg	Val	Ala	Ala	Ile 105	Tyr	Gly	Glu	Lys	Arg 110	Thr	Thr
Val	Val	Leu 115	Asn	Asn	Gly	Ala	Ala 120	Ser	Glu	Val	Tyr	Phe 125	Pro	Ala	Gly
Asp	Ser 130	Phe	Val	Asp	Ile	Ala 135	Ala	Gly	Gln	Val	Leu 140	Leu	Asn	Gln	Gly
Asp 145	Asn	Thr	Ile	Asp	Ile 150	Val	Asn	Asn	Trp	Gly 155	Trp	Tyr	Leu	Ile	Asp 160
Ser	Ile	Thr	Ile	Thr 165	Pro	Ser	Ala	Pro	Arg 170	Pro	Pro	His	Gln	Ile 175	Asn
Pro	Ser	Pro	Val 180	Asn	Pro	Ala	Ala	Asp 185	Asp	Asn	Ala	Arg	Ala 190	Leu	Tyr
Ala	Tyr	Leu 195	Arg	Ser	Ile	Tyr	Gly 200	Lys	Lys	Ile	Leu	Ser 205	Gly	Gln	Gln
Glu 210	Leu	Ser	Trp	Ala	Asn	Trp 215	Ile	Ala	Gln	Gln	Thr 220	Gly	Lys	Thr	Pro
Ala 225	Leu	Val	Ser	Val	Asp 230	Met	Met	Asp	Tyr	Ser 235	Pro	Ser	Arg	Val	Glu 240
Arg	Gly	Thr	Val	Gly 245	Ser	Ala	Val	Glu	Glu	Ala 250	Ile	Glu	His	His 255	Arg
Arg	Gly	Gly	Ile 260	Val	Ser	Val	Leu	Trp 265	His	Trp	Asn	Ala	Pro 270	Thr	Gly
Leu	Tyr	Asp 275	Thr	Pro	Glu	Arg	Arg 280	Trp	Trp	Ser	Gly	Phe 285	Tyr	Thr	Asp
Ala 290	Thr	Asp	Phe	Asp	Val	Ala 295	Arg	Ala	Leu	Ala	Asp 300	Thr	Thr	Asn	Ala
Asn 305	Tyr	Thr	Leu	Leu	Ile 310	Arg	Asp	Ile	Asp	Ala 315	Ile	Ala	Val	Gln	Leu 320
Lys	Arg	Leu	Arg	Asp 325	Ala	Gly	Val	Pro	Val 330	Leu	Trp	Arg	Pro	Leu 335	His
Glu	Ala	Glu	Gly 340	Gly	Trp	Phe	Trp	Trp 345	Gly	Ala	Lys	Gly	Pro 350	Glu	Ala
Tyr	Lys	Lys 355	Leu	Trp	Gly	Ile	Leu 360	Tyr	Asp	Arg	Leu	Thr 365	Asn	Tyr	His
Gly 370	Leu	Asn	Asn	Leu	Leu	Trp 375	Val	Trp	Asn	Ser	Ile 380	Leu	Pro	Glu	Trp
Tyr 385	Pro	Gly	Asp	Glu	Thr 390	Val	Asp	Ile	Val	Ser 395	Ala	Asp	Val	Tyr	Ala 400
Gln	Gly	Asn	Gly	Pro 405	Met	Ser	Thr	Gln	Tyr 410	Asn	Gln	Leu	Ile	Glu 415	Leu

Gly Lys Asp Lys Lys Met Ile Ala Ala Thr Glu Val Gly Ala Ala Pro  
 420 425 430  
 Leu Pro Asp Leu Leu Gln Ala Tyr Glu Ala His Trp Leu Trp Phe Ala  
 435 440 445  
 Val Trp Gly Asp Thr Phe Ile Asn Asn Pro Gln Trp Asn Ser Ile Glu  
 450 455 460  
 Thr Leu Lys Thr Ile Tyr Asn Ser Asp Tyr Val Leu Thr Leu Asp Glu  
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 Ile Gln Gly Trp Arg Asn Ala Gln  
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<210> 15  
 <211> 1107  
 <212> DNA  
 <213> Bacillus sp. AA349

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 caagctgaag cacctggaaa aacggctgaa aatggagtct gggataaagt tcgaaataat 180  
 cctggaaaaag ccaatcctcc agcaggaaaa gtcaatgggt tttatataga tggaacaacc 240  
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 gcttttaatcg gaaaagagga caaagtaatt attaacattt ctaatgaatg gtttggttct 600  
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<210> 16  
 <211> 369  
 <212> PRT  
 <213> Bacillus sp. AA349

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 Met His Lys Val Pro Trp Ala Pro Gln Ala Glu Ala Pro Gly Lys Thr  
 35 40 45  
 Ala Glu Asn Gly Val Trp Asp Lys Val Arg Asn Asn Pro Gly Lys Ala  
 50 55 60  
 Asn Pro Pro Ala Gly Lys Val Asn Gly Phe Tyr Ile Asp Gly Thr Thr  
 65 70 75 80  
 Leu Tyr Asp Ala Asn Gly Lys Pro Phe Val Met Arg Gly Ile Asn His  
 85 90 95

Gly His Ser Trp Tyr Lys Pro His Ile Glu Thr Ala Met Glu Ala Ile  
 100 105 110  
 Ala Asp Thr Gly Ala Asn Ser Ile Arg Val Val Leu Ser Asp Gly Gln  
 115 120 125  
 Gln Trp Thr Lys Asp Asp Val Asp Glu Val Ala Lys Ile Ile Ser Leu  
 130 135 140  
 Ala Glu Lys His Ser Leu Val Ala Ala Leu Glu Val His Asp Ala Leu  
 145 150 155 160  
 Gly Thr Asp Asp Ile Glu Pro Leu Leu Lys Thr Val Asp Tyr Trp Ile  
 165 170 175  
 Glu Ile Lys Asp Ala Leu Ile Gly Lys Glu Asp Lys Val Ile Ile Asn  
 180 185 190  
 Ile Ser Asn Glu Trp Phe Gly Ser Trp Ser Ser Glu Gly Trp Ala Asp  
 195 200 205  
 Gly Tyr Lys Lys Ala Ile Pro Leu Leu Arg Glu Ala Gly Leu Lys His  
 210 215 220  
 Thr Leu Met Val Asp Ala Ala Gly Trp Gly Gln Phe Pro Arg Ser Ile  
 225 230 235 240  
 His Glu Lys Gly Leu Glu Val Phe Asn Ser Asp Pro Leu Lys Asn Thr  
 245 250 255  
 Met Phe Ser Ile His Met Tyr Glu Trp Ala Ala Gly Asn Pro Gln Gln  
 260 265 270  
 Val Lys Asp Asn Ile Asp Gly Val Leu Glu Lys Asn Leu Ala Val Val  
 275 280 285  
 Ile Gly Glu Phe Gly His His His Tyr Gly Arg Asp Val Ala Val Asp  
 290 295 300  
 Thr Ile Leu Ser His Ser Glu Lys Tyr Asp Val Gly Trp Leu Ala Trp  
 305 310 315 320  
 Ser Trp His Gly Asn Ser Gly Gly Val Glu Tyr Leu Asp Leu Ala Thr  
 325 330 335  
 Asp Phe Ser Gly Thr Gln Leu Thr Glu Trp Gly Glu Arg Ile Val His  
 340 345 350  
 Gly Pro Asn Gly Leu Lys Glu Thr Ser Glu Ile Val Ser Val Tyr Lys  
 355 360 365

Lys

<210> 17  
 <211> 915  
 <212> DNA  
 <213> Bacillus sp.

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 cgcaatgtta tggtctccat acacatgtac ggttcctgga ataatcagtc gcgaatcggc 180  
 agcgaattgc aggccatcaa agaccttggt cttgctgtca tgattggtga attcggatac 240  
 aactacaaca acggcaataa caacttgggg agtcagggtta acgccagga aatcatgaat 300



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caggcgcaag caaaaggaat cggctacatg ccgtgggtcgt ggactggcaa tgacgogggt 360
aactcttggg tggatatgac aacaaacgat tggcaaacac ttacatcatg ggggaatcta 420
gttgtaaatg gaaccaacgg cattcgagct acgtctgtcc cagcaactgt atttaataca 480
caaacaacaa tttatgattt tgaaggcggc aatgcccgagg gctggtcagg ttccgggttg 540
agcggggggc cttgggtctgt taatgaatgg gcggcgagcg gtagttattc tctcaaagcg 600
aatatatctc taggcgccac tcaaaaagct ttgcaaacca cagcgtccca taatttcagc 660
ggccggtcta cattatccgt aagagtaaag catgcagcat ggggaaatca cggcagcggt 720
atgcaagcca agttatatgt gaaaacaggg gccgggttacg cctgggtatga tggcggcact 780
gtaaacaatca acagctcggg caacacattg acgctaaacc tggcagggcat tcctaactctg 840
aacgacgtca gagaactcgg aattgaattt ataacacctg caaattcgag tggttctttc 900
gcaatttatg ttgac 915

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<210> 18  
 <211> 305  
 <212> PRT  
 <213> Bacillus sp.

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<400> 18
Ile Ser Thr Leu Arg Asn Ala Gly Ile Arg Asn Thr Ile Val Val Asp
  1                      5                      10                      15

Ala Ser Gly Trp Gly Gln Asn Ser Ser Pro Ile Lys Ala Tyr Gly Asn
      20                      25                      30

Glu Val Leu Asn His Asp Pro Gln Arg Asn Val Met Phe Ser Ile His
      35                      40                      45

Met Tyr Gly Ser Trp Asn Asn Gln Ser Arg Ile Gly Ser Glu Leu Gln
      50                      55                      60

Ala Ile Lys Asp Leu Gly Leu Ala Val Met Ile Gly Glu Phe Gly Tyr
      65                      70                      75                      80

Asn Tyr Asn Asn Gly Asn Asn Asn Leu Gly Ser Gln Val Asn Ala Gln
      85                      90                      95

Glu Ile Met Asn Gln Ala Gln Ala Lys Gly Ile Gly Tyr Met Pro Trp
      100                      105                      110

Ser Trp Thr Gly Asn Asp Ala Ala Asn Ser Trp Leu Asp Met Thr Thr
      115                      120                      125

Asn Asp Trp Gln Thr Leu Thr Ser Trp Gly Asn Leu Val Val Asn Gly
      130                      135                      140

Thr Asn Gly Ile Arg Ala Thr Ser Val Pro Ala Thr Val Phe Asn Thr
      145                      150                      155                      160

Gln Thr Thr Ile Tyr Asp Phe Glu Gly Gly Asn Ala Gln Gly Trp Ser
      165                      170                      175

Gly Ser Gly Leu Ser Gly Gly Pro Trp Ser Val Asn Glu Trp Ala Ala
      180                      185                      190

Ser Gly Ser Tyr Ser Leu Lys Ala Asn Ile Ser Leu Gly Ala Thr Gln
      195                      200                      205

Lys Ala Leu Gln Thr Thr Ala Ser His Asn Phe Ser Gly Arg Ser Thr
      210                      215                      220

Leu Ser Val Arg Val Lys His Ala Ala Trp Gly Asn His Gly Ser Gly
      225                      230                      235                      240

Met Gln Ala Lys Leu Tyr Val Lys Thr Gly Ala Gly Tyr Ala Trp Tyr
      245                      250                      255

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Asp Gly Gly Thr Val Asn Ile Asn Ser Ser Gly Asn Thr Leu Thr Leu  
                   260                                  265                                  270

Asn Leu Ala Gly Ile Pro Asn Leu Asn Asp Val Arg Glu Leu Gly Ile  
                   275                                  280                                  285

Glu Phe Ile Thr Pro Ala Asn Ser Ser Gly Ser Phe Ala Ile Tyr Val  
                   290                                  295                                  300

Asp  
 305

<210> 19  
 <211> 397  
 <212> DNA  
 <213> *Bacillus clausii*

<400> 19  
 atctctcagg gcttggtagg agtcattatt ctcttataca tggcatttag tcaagagaga 60  
 ggattggcgc aaactggatt tcaagtaaca gggacccagt tgcttgatgg agagggcaat 120  
 ccgtatgtga tgcgtggagt caatcacgga cattcatggt tcaaacaaga ccttgataca 180  
 gcaataccag ctattgcagc gactggcgct aatacgggtga gaatcgtttt atcgaatggc 240  
 caacaatggg agcgagatac cgtagcggaa gttgaaagag tgcttgcagt taccgaagag 300  
 gaaggcttga cggctgtact tgaagtccat gatgcgacgg gaagtgatga tccaaacgat 360  
 ttgtttactg cagtggagta ttggtcagag agaggat . 397

<210> 20  
 <211> 132  
 <212> PRT  
 <213> *Bacillus clausii*

<400> 20  
 Ile Ser Gln Gly Leu Val Gly Val Ile Ile Leu Leu Tyr Met Ala Phe  
   1                  5                                  10                                  15

Ser Gln Glu Arg Gly Leu Ala Gln Thr Gly Phe Gln Val Thr Gly Thr  
                   20                                  25                                  30

Gln Leu Leu Asp Gly Glu Gly Asn Pro Tyr Val Met Arg Gly Val Asn  
                   35                                  40                                  45

His Gly His Ser Trp Phe Lys Gln Asp Leu Asp Thr Ala Ile Pro Ala  
                   50                                  55                                  60

Ile Ala Ala Thr Gly Ala Asn Thr Val Arg Ile Val Leu Ser Asn Gly  
                   65                                  70                                  75                                  80

Gln Gln Trp Glu Arg Asp Thr Val Ala Glu Val Glu Arg Val Leu Ala  
                   85                                  90                                  95

Val Thr Glu Glu Gly Leu Thr Ala Val Leu Glu Val His Asp Ala  
                   100                                  105                                  110

Thr Gly Ser Asp Asp Pro Asn Asp Leu Phe Thr Ala Val Glu Tyr Trp  
                   115                                  120                                  125

Ser Glu Arg Gly  
                   130

<210> 21  
 <211> 960  
 <212> DNA  
 <213> Bacillus sp.

<400> 21  
 atgaatcgta agcgggttaca atggggttgga gcactagtgg tgggtgttggt tttgtttgta 60  
 tacagtagcg gtttagcatc tgcacaaagc ggctttcacg taaaagggtac agagttgttg 120  
 gacaaaaatg gcgatcctta cgttatgcgt ggcgtcaacc atggacattc ttgggtttaa 180  
 caagattttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240  
 gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300  
 gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360  
 gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420  
 aagggggacag aagaccgggt aatcattaac attgccaatg aatgggtatgg ggcgtggagg 480  
 agtgacgttt gggcagaggc atacgcacaa gcgatcccg ccttgccgag tgctggcctc 540  
 gcccatagc taatagttga tgcggcaggt tggggacagt accctgcctc tatccatgag 600  
 cgggggagccg acgtatttgc ctccgatcca ttaaaaaaca caatgttttc catccatag 660  
 tacgaatatg caggagcggg tagggcgaca gtttctgaaa acatcgacgg tgtacttgct 720  
 gaaaatcttg ctgtggtaat cgggtgaattt ggccataggc atcatgatgg cgatgtcgat 780  
 gaagatgcga ttttggccta tacagcagag cggcaagtgg gctggcctgc ctgggtcatg 840  
 tatggcaata gcgggggtgt tgaatacttg gatttaactg aaggcccatc aggtccatta 900  
 acgagttggg gcgaacggat tgtctatggg gaaatgggct taaaagtaat tgatcacttg 960

<210> 22  
 <211> 320  
 <212> PRT  
 <213> Bacillus sp.

<400> 22  
 Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Val Val Leu  
 1 5 10 15  
 Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe  
 20 25 30  
 His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val  
 35 40 45  
 Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu  
 50 55 60  
 Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile  
 65 70 75 80  
 Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu  
 85 90 95  
 Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu  
 100 105 110  
 Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys  
 115 120 125  
 Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu  
 130 135 140  
 Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg  
 145 150 155 160  
 Ser Asp Val Trp Ala Glu Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg  
 165 170 175  
 Ser Ala Gly Leu Ala His Thr Leu Ile Val Asp Ala Ala Gly Trp Gly  
 180 185 190

Gln Tyr Pro Ala Ser Ile His Glu Arg Gly Ala Asp Val Phe Ala Ser  
 195 200 205

Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met Tyr Glu Tyr Ala  
 210 215 220

Gly Ala Asp Arg Ala Thr Val Ser Glu Asn Ile Asp Gly Val Leu Ala  
 225 230 235 240

Glu Asn Leu Ala Val Val Ile Gly Glu Phe Gly His Arg His His Asp  
 245 250 255

Gly Asp Val Asp Glu Asp Ala Ile Leu Ala Tyr Thr Ala Glu Arg Gln  
 260 265 270

Val Gly Trp Leu Ala Trp Ser Trp Tyr Gly Asn Ser Gly Gly Val Glu  
 275 280 285

Tyr Leu Asp Leu Thr Glu Gly Pro Ser Gly Pro Leu Thr Ser Trp Gly  
 290 295 300

Glu Arg Ile Val Tyr Gly Glu Met Gly Leu Lys Val Ile Asp His Leu  
 305 310 315 320

<210> 23  
 <211> 564  
 <212> DNA  
 <213> Bacillus sp.

<400> 23  
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 tacagtagcg gtttagcatc tgcacaaaagc ggcttttcacg taaaagggtac agagttgttg 120  
 gacaaaaaatg gcgatcctta cgttatgcgt ggcggtcaacc atggacattc ttggttttaa 180  
 caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240  
 gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300  
 gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360  
 gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420  
 aagggggacag aagaccgggt aatcattaac attgccaatg aatgggtatgg ggcgtggagg 480  
 agtgaccttt gggcaaaagc atacgcacaa gcgatcccg cgttgccgag tgctggcctc 540  
 gcccatacgt taataattga tgcc 564

<210> 24  
 <211> 188  
 <212> PRT  
 <213> Bacillus sp.

<400> 24  
 Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Ala Val Leu  
 1 5 10 15

Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe  
 20 25 30

His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val  
 35 40 45

Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu  
 50 55 60

Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile  
 65 70 75 80

Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu  
85 90 95

Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu  
100 105 110

Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys  
115 120 125

Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu  
130 135 140

Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg  
145 150 155 160

Ser Asp Leu Trp Ala Lys Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg  
165 170 175

Ser Ala Gly Leu Ala His Thr Leu Ile Ile Asp Ala  
180 185

<210> 25  
<211> 2445  
<212> DNA  
<213> Bacillus sp.

<400> 25  
atgaacaaac aaccgttaaa gactgcattt attatgttgt tatgtagcgt gtttatgttt 60  
caaagcctac cttactatgt gaacgctatc aatgaaggcg agagagaagc ttttgcattcc 120  
gcaggagat atgatgctga acaggcgact acgacaggaa atgccgtatt caccgaccgag 180  
cctgttgagg acggcgagta cgccgggtccg ggctacattt cttctttttc tgaagattcc 240  
tcgccacctt cttcatcgac aacctttcac attcaggccg ataaaacgga gctctatcat 300  
ttatctatcg gatactatgc tccatacggg aacaagggaa ccacaattct ggtgaacggg 360  
gcaggtaacg gagagtttat gttgccagcg cccgaggacg gggcagtcct cgccgaagtg 420  
gaaattagca aaatcctgct cgaagaagga aataatacga ttacattcac aagaggctgg 480  
ggttattacg gcattgaata tattcgggtc gagccgggta atccaacgtt accgactata 540  
tttattgaag cagaagaaga ttacgaagcg actggaaatg ttagcggtac caatgaaatc 600  
gaagggttatt ccggagcagg ctatgtgttc aaccaagagg ggacaattca ttggaatgta 660  
acctcaccgg aaacctctat atatgaagta atcggtgcct atgcagctcc ttatggcgac 720  
aaacaaacaa atctgacagt gaatggacag ggtaccgtca atcttgactt gaaagagaca 780  
gaagtcttcg tggagttgaa tgtcggcatc gtaagtctca atgaaggcga aaacacacta 840  
acactccata gtggttgggg atggtacaat atcgattata tcaagcttgt acctgtgggtc 900  
agttcggatc ccgaaccgca tcaggtcgaa aaaacactgg tgaatccgga cgccctacact 960  
gaggcaagag cgctaattaa ttatctcgta gaccagtacg ggaacaaaat tctatcaggt 1020  
caaaccgagt tgaagacgc caggtggatc catgaacagg tgggcaaata tctgcgggt 1080  
atggcagttg attttatgga ctacagcccg tcccgcgtag tgcattggcg aactgggaact 1140  
gcggttgagg aagcgattga gtgggcagag atgggtggga tcattacctt ccactggcat 1200  
tggaacgcgc caaaggacct gcttaatgta cccggcaatg agtgggtggtc cgggtttttat 1260  
acccgtgcca caacgtttga tgtggagtac gcttttagaga accgggaatc tgaggatttc 1320  
caattgttga ttagcgacat ggatgtgac gccgagcaat tgaagcggct gcaggcagag 1380  
aacatccctg tggtatggag accgcttcat gaggcggaag gcggctgggt ctggtggggc 1440  
gccaaaggtc cagaggcggc aatagagctc tacaggctga tgtacgatcg ttacaccaat 1500  
caccataaac taaacaattt gatatggatg tggaaatcgg aagcggaaga atggtatccg 1560  
ggcgatgatg tcgtggacat gatcagtaac gatatttata atcctgtcgg agatttcagt 1620  
cccagcatga acaagtatga gcatctaaag gaattgggtac aggataagaa gctggttgcc 1680  
ttgcctgaaa ccggcattat tccggatccc gatcagcttc agctgttcaa tgcgaactgg 1740  
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cacctgcaaa aggtgtttca tcatgactac gtcacacccc tggatgaatt gccggagaa 1860  
ctgtcccgtt acggattatc tgaaggagtc tgggaagacg acgccgatct atccgtaaaa 1920  
acgaggacga cctccgaat tacagtgaac tggtaaaatg ccattcaata tgattccgtt 1980  
aatggctata aattaattaa agatgggtgta gagaccgttt cagttgaagg cggcgtgcaa 2040  
gagtatacct tcacaaattt attgccgggc acgcagtata cgataaaagt agaggcactg 2100  
gaccaggatg accgatggac cgccgacgga cgggtcgccg ttgtatctac attatccaac 2160  
gctccgatat cctatcctcc ggctgtcact cctgatgagc cgaatgaaga actgtcggag 2220  
ggagagtata cgctcttggc agatgactta tccagccagg atgggtgttct ggaagtaagt 2280

cttgagccga cagttacgaa gctcattatt ccttctgcac tagccggcac attagacgga 2340  
 gacttgagaa tcggttatgg ggacgtctgg atcgatcatcc cacacgaaca gcttgggggt 2400  
 gacgagcagc aatccggcag cgcgtatgag ttagtgctgg agatc 2445

<210> 26  
 <211> 815  
 <212> PRT  
 <213> Bacillus sp.

<400> 26  
 Met Asn Lys Gln Pro Leu Lys Thr Ala Phe Ile Met Leu Leu Cys Ser  
   1                  5                  10                  15  
 Val Phe Met Phe Gln Ser Leu Pro Tyr Tyr Val Asn Ala Ile Asn Glu  
           20                  25                  30  
 Gly Glu Arg Glu Ala Phe Ala Ser Ala Gly Arg Tyr Asp Ala Glu Gln  
           35                  40                  45  
 Ala Thr Thr Thr Gly Asn Ala Val Phe Thr Thr Glu Pro Val Glu Asp  
   50                  55                  60  
 Gly Glu Tyr Ala Gly Pro Gly Tyr Ile Ser Phe Phe Ser Glu Asp Ser  
   65                  70                  75                  80  
 Ser Pro Pro Ser Ser Ser Thr Thr Phe His Ile Gln Ala Asp Lys Thr  
           85                  90                  95  
 Glu Leu Tyr His Leu Ser Ile Gly Tyr Tyr Ala Pro Tyr Gly Asn Lys  
           100                  105                  110  
 Gly Thr Thr Ile Leu Val Asn Gly Ala Gly Asn Gly Glu Phe Met Leu  
   115                  120                  125  
 Pro Ala Pro Glu Asp Gly Ala Val Ser Ala Glu Val Glu Ile Ser Lys  
   130                  135                  140  
 Ile Leu Leu Glu Glu Gly Asn Asn Thr Ile Thr Phe Thr Arg Gly Trp  
  145                  150                  155                  160  
 Gly Tyr Tyr Gly Ile Glu Tyr Ile Arg Val Glu Pro Val Asn Pro Thr  
           165                  170                  175  
 Leu Pro Thr Ile Phe Ile Glu Ala Glu Glu Asp Tyr Glu Ala Thr Gly  
   180                  185                  190  
 Asn Val Ser Val Thr Asn Glu Ile Glu Gly Tyr Ser Gly Ala Gly Tyr  
   195                  200                  205  
 Leu Phe Asn Gln Glu Gly Thr Ile His Trp Asn Val Thr Ser Pro Glu  
   210                  215                  220  
 Thr Ser Ile Tyr Glu Val Ile Val Ala Tyr Ala Ala Pro Tyr Gly Asp  
  225                  230                  235                  240  
 Lys Gln Thr Asn Leu Thr Val Asn Gly Gln Gly Thr Val Asn Leu Asp  
           245                  250                  255  
 Leu Lys Glu Thr Glu Val Phe Val Glu Leu Asn Val Gly Ile Val Ser  
   260                  265                  270  
 Leu Asn Glu Gly Glu Asn Thr Leu Thr Leu His Ser Gly Trp Gly Trp  
   275                  280                  285  
 Tyr Asn Ile Asp Tyr Ile Lys Leu Val Pro Val Val Ser Ser Asp Pro  
   290                  295                  300

Glu	Pro	His	Gln	Val	Glu	Lys	Thr	Leu	Val	Asn	Pro	Asp	Ala	Ser	Pro	
305					310					315					320	
Glu	Ala	Arg	Ala	Leu	Ile	Asn	Tyr	Leu	Val	Asp	Gln	Tyr	Gly	Asn	Lys	
				325					330					335		
Ile	Leu	Ser	Gly	Gln	Thr	Glu	Leu	Lys	Asp	Ala	Arg	Trp	Ile	His	Glu	
			340					345					350			
Gln	Val	Gly	Lys	Tyr	Pro	Ala	Val	Met	Ala	Val	Asp	Phe	Met	Asp	Tyr	
		355					360					365				
Ser	Pro	Ser	Arg	Val	Val	His	Gly	Ala	Thr	Gly	Thr	Ala	Val	Glu	Glu	
	370					375					380					
Ala	Ile	Glu	Trp	Ala	Glu	Met	Gly	Gly	Ile	Ile	Thr	Phe	His	Trp	His	
385					390					395					400	
Trp	Asn	Ala	Pro	Lys	Asp	Leu	Leu	Asn	Val	Pro	Gly	Asn	Glu	Trp	Trp	
				405					410					415		
Ser	Gly	Phe	Tyr	Thr	Arg	Ala	Thr	Thr	Phe	Asp	Val	Glu	Tyr	Ala	Leu	
			420					425					430			
Glu	Asn	Arg	Glu	Ser	Glu	Asp	Phe	Gln	Leu	Leu	Ile	Ser	Asp	Met	Asp	
		435					440					445				
Val	Ile	Ala	Glu	Gln	Leu	Lys	Arg	Leu	Gln	Ala	Glu	Asn	Ile	Pro	Val	
	450					455					460					
Leu	Trp	Arg	Pro	Leu	His	Glu	Ala	Glu	Gly	Gly	Trp	Phe	Trp	Trp	Gly	
465					470					475					480	
Ala	Lys	Gly	Pro	Glu	Ala	Ala	Ile	Glu	Leu	Tyr	Arg	Leu	Met	Tyr	Asp	
				485					490					495		
Arg	Tyr	Thr	Asn	His	His	Lys	Leu	Asn	Asn	Leu	Ile	Trp	Met	Trp	Asn	
			500					505					510			
Ser	Glu	Ala	Glu	Glu	Trp	Tyr	Pro	Gly	Asp	Asp	Val	Val	Asp	Met	Ile	
		515					520					525				
Ser	Thr	Asp	Ile	Tyr	Asn	Pro	Val	Gly	Asp	Phe	Ser	Pro	Ser	Ile	Asn	
	530					535					540					
Lys	Tyr	Glu	His	Leu	Lys	Glu	Leu	Val	Gln	Asp	Lys	Lys	Leu	Val	Ala	
545					550					555					560	
Leu	Pro	Glu	Thr	Gly	Ile	Ile	Pro	Asp	Pro	Asp	Gln	Leu	Gln	Leu	Phe	
				565					570					575		
Asn	Ala	Asn	Trp	Ser	Trp	Phe	Ala	Thr	Trp	Thr	Gly	Asp	Tyr	Ile	Arg	
			580					585					590			
Asp	Gly	Ile	Ser	Asn	Pro	Ile	Glu	His	Leu	Gln	Lys	Val	Phe	His	His	
		595					600					605				
Asp	Tyr	Val	Ile	Thr	Leu	Asp	Glu	Leu	Pro	Glu	Asn	Leu	Ser	Arg	Tyr	
	610					615					620					
Gly	Leu	Ser	Glu	Gly	Val	Trp	Lys	Ser	Asp	Ala	Asp	Leu	Ser	Val	Lys	
625					630					635					640	
Thr	Arg	Thr	Thr	Ser	Glu	Ile	Thr	Val	Asn	Trp	Ser	Asn	Ala	Ile	Gln	
				645					650					655		

Tyr Asp Ser Val Asn Gly Tyr Lys Leu Ile Lys Asp Gly Val Glu Thr  
 660 665 670  
 Val Ser Val Glu Gly Gly Val Gln Glu Tyr Thr Phe Thr Asn Leu Leu  
 675 680 685  
 Pro Gly Thr Gln Tyr Thr Ile Lys Val Glu Ala Leu Asp Gln Asp Asp  
 690 695 700  
 Arg Trp Thr Ala Asp Gly Pro Val Ala Val Val Ser Thr Leu Ser Asn  
 705 710 715 720  
 Ala Pro Ile Ser Tyr Pro Pro Ala Val Thr Pro Asp Glu Pro Asn Glu  
 725 730 735  
 Glu Leu Ser Glu Gly Glu Tyr Thr Leu Leu Ala Asp Asp Leu Ser Ser  
 740 745 750  
 Gln Asp Gly Val Leu Glu Val Ser Leu Glu Pro Thr Val Thr Lys Leu  
 755 760 765  
 Ile Ile Pro Ser Ala Leu Ala Gly Thr Leu Asp Gly Asp Leu Arg Ile  
 770 775 780  
 Gly Tyr Gly Asp Val Trp Ile Val Ile Pro His Glu Gln Leu Gly Gly  
 785 790 795 800  
 Asp Glu Gln Gln Ser Gly Ser Ala Tyr Glu Leu Val Leu Glu Ile  
 805 810 815

<210> 27  
 <211> 1488  
 <212> DNA  
 <213> Bacillus sp.

<400> 27  
 atgaggaatg aaaaaatcag gccatttact aaaataaagg caagtgttgt tactagtgtt 60  
 ttactattaa ctatttccct aattttcact ataggaata tagcaaatgc tgaatctgag 120  
 gtaagaatat ttgaagctga agatgctatt ttaaattgggc tgactattaa aaattctgaa 180  
 ccagggtttt ctggtaccgg atatgtagg gactttgaaa atagctctca gagggtgacg 240  
 tttcaaatg aggcctctaa agccggttta tacaacttaa atattggata tggcgcgatt 300  
 tatggaagtg gaaaagtagc taatgttatt gtaaattggag agaagctaag tacttttaca 360  
 atgggaagtg gctttggtaa agcgtcagca ggaaaggat tacttaattc aggcctaaat 420  
 actatctcga ttactcctaa ttggacatgg tttaccattg attatattga agttatacat 480  
 gcaccggaac cggaaaacca taatgtagaa aagacgttaa ttaaccctaa tgcaacggat 540  
 gaagccaaag cttaataaag ctatctagtt gataactttg gtgagaaaat tcttgccagg 600  
 caacatgatt atccaaatac acgaccacga gatttagaat atatttatga aactactggg 660  
 aagtatcctg ctgttttagg tttagacttt attgataaca gtccttctag agttgagcgc 720  
 ggagcctctg ctgatgaaac accagtagct attgactggt ggaataaagg ggggaattgtt 780  
 actttcacct ggcattggaa tgctcccaaa gatttattag atgaaccagg aaatgaatgg 840  
 tggagtgggt tttatacgag agcaacaact tttgacgtag aatatgcttt aaaacatccg 900  
 aagtcggagg actacatgct tctaatacgt gatattgat taatagctgg tgaactaaag 960  
 aaattgcagg aagcaaatgt tcctgtttta tggaggccac ttcattgaggc tgaaggcggg 1020  
 tggttctggt ggggggcaaa aggtcctgaa tcaaccaagg agctatggag ataatgtat 1080  
 gatagaatga cgaactacca taacttaa attttaatat gggatggaa ttccattgaa 1140  
 gaggattggt atcctggaga tgagtatgtc gatattgtaa gcttcgattc atatccagg 1200  
 gaataaact atagtccaat gagccgtgag tatgaagcac ttaaagagtt gtctagtaac 1260  
 aagaaactta tagcaatagc agaaaatgga ccaataccag atcctgattt actacaactt 1320  
 taccatgcta actatagttg gtttgctaca tggaatggag atatattaag aaatcaaat 1380  
 agcgaagagc acctaagaaa agtataaat catgattatg tgattaccct aaataaatta 1440  
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<210> 28  
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 <213> Bacillus sp.

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 Phe Gln Ile Glu Ala Pro Lys Ala Gly Leu Tyr Asn Leu Asn Ile Gly  
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 Tyr Gly Ala Ile Tyr Gly Ser Gly Lys Val Ala Asn Val Ile Val Asn  
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 Gly Glu Lys Leu Ser Thr Phe Thr Met Gly Ser Gly Phe Gly Lys Ala  
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 Thr Pro Asn Trp Thr Trp Phe Thr Ile Asp Tyr Ile Glu Val Ile His  
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 Ala Pro Glu Pro Glu Asn His Asn Val Glu Lys Thr Leu Ile Asn Pro  
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 Phe Gly Glu Lys Ile Leu Ala Gly Gln His Asp Tyr Pro Asn Thr Arg  
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 Pro Arg Asp Leu Glu Tyr Ile Tyr Glu Thr Thr Gly Lys Tyr Pro Ala  
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 Val Leu Gly Leu Asp Phe Ile Asp Asn Ser Pro Ser Arg Val Glu Arg  
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 Gly Ala Ser Ala Asp Glu Thr Pro Val Ala Ile Asp Trp Trp Asn Lys  
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 Gly Gly Ile Val Thr Phe Thr Trp His Trp Asn Ala Pro Lys Asp Leu  
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 Leu Asp Glu Pro Gly Asn Glu Trp Trp Ser Gly Phe Tyr Thr Arg Ala  
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<210> 31

<211> 3041

<212> DNA

<213> Caldocellulosiruptor sp.

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Thr Gly Ser Lys Tyr Asn Asp Glu Trp Asn Asp Asn His Met Leu Arg  
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&lt;213&gt; Bacillus sp. I633

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&lt;213&gt; Bacillus sp. AAI12

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ugccggugau	aaaccggagg	aagguggggg	ugacgucaaa	ucaucaugcc	ccuuauagacc	1200
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aaauugcuagu	aaucgcggau	cagcaugccg	cggugaauac	guucccgggc	cuuguacaca	1380
ccgcccguca	caccacgaga	guuuguaaca	cccgaagucg	guggaguaac	ccuuacggga	1440
gcuagccgccc	uaagguggga	cagaugauug	gggugaaguc	guaacaaggu	agccguaucc	1500
gaaggugc						1508